MO2

HERD IMMUNITY AS A RESULT IN DYNAMIC AGENT-BASED EPIDEMIC MODELS

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OBJECTIVES: Herd immunity describes a phenomenon in the area of communicable diseases. Pathogens are spread by infected persons. Protecting a part of the population—for example via vaccination—lowers the overall appearance of pathogens as these people cannot spread pathogens any more. Not protected people profit by fewer contacts with pathogens, and further, a lower number of infections for them can be expected. Classic Markov model cannot provide herd immunity as a result. In this work, we propose calculations of herd immunity, create a model that is able to simulate epidemics, and show herd immunity dynamically in different states of the model. Appearance of herd immunity is very disputed because it 1) cannot be measured directly in real life and 2) depends on several factors. **METHODS:** Classic Markov models require herd immunity as a static input parameter that cannot be provided. The developed agent-based model includes single persons with different infection states and a single pathogen. Every agent is part of a social contact model. It is possible to simulate scenarios without vaccinations and with different vaccination strategies. Herd immunity as a result of the dynamic model is calculated as the reduction of the carrier rate of nonvaccinated persons for a certain vaccination strategy compared with the scenario without vaccinations. **RESULTS:** Results show herd immunity as simulation result depending not only on vaccination strategies but also on other system parameters. Further work extends the social contact structure with places like households, schools, or workplaces that are expected to have an impact on herd immunity as well. **CONCLUSIONS:** Results can be implemented in systems for calculating new strategies for vaccination programs. Current work considers two or more concurrent serotypes where herd immunity and serotype replacement affects each other. In this case, different definitions of herd immunity are possible.

MO3

THE DEVELOPMENT AND VALIDATION OF A DECISION MODEL REPRESENTING THE FULL DISEASE COURSE OF ACUTE MYELOID LEUKEMIA

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OBJECTIVES: Acute myeloid leukemia (AML) is a heterogeneous disease, consisting of several subtypes with a variety in prognosis. a new genomics technology, the AML profiler, has been developed that identifies new genetic subtypes. Since no decision model exists that describes the full disease course of AML, the potential cost-effectiveness of this test cannot yet be determined. The aim of this study is to fill this gap and develop and validate a disease progression model for AML. **METHODS:** The structure of the model and the identification of relevant parameters were based on the literature and expert opinion. All input parameters were estimated from clinical trial data (HOVON data) for patients aged 18 to 60 years. The internal and external validity of the model was evaluated by comparing model-based survival results with the results from HOVON trials and the literature. **RESULTS:** Important prognostic factors for AML were derived from the literature and expert opinion a microsimulation model (i.e., individual patient sampling) was designed to incorporate all important prognostic factors in the model. The prognostic factors were included as covariates in parametric survival functions for two events: relapse and death. The model combined those survival functions with individual patient data to calculate life-years per patient. The average 5-year survival of the simulated patient cohort was 40%, which is similar to the survival found in HOVON trials and the literature. **DISCUSSION:** The content validity of the model was achieved by involving clinical experts in the construction of the model. The survival estimated using the model corresponds with those seen elsewhere, suggesting an acceptable level of internal and external validity. Therefore, the model can be used to assess the cost-effectiveness of AML genomics technologies such as the AML profiler. Moreover, the model can be used for other cost-effectiveness analyses in the field of AML.

MO4

USING AHP WEIGHTS TO FILL MISSING GAPS IN MARKOV DECISION MODELS

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OBJECTIVES: We propose to combine the versatility of the analytic hierarchy process (AHP) with the decision-analytic sophistication of health-economic modeling in a new methodology for early technology assessment. As an illustration, we apply this methodology to a new technology to diagnose breast cancer. **METHODS:** The AHP is a technique for multicriteria analysis, relatively new in the field of technology assessment. It can integrate both quantitative and qualitative criteria in the assessment of alternative technologies. We applied the AHP to prioritize a more versatile set of outcome measures than most Markov models do. These outcome measures include clinical effectiveness and costs, but also weighted estimates of patient comfort and safety. Furthermore, as no clinical data are available for this technology yet, the AHP is applied to predict the performance of the new technology with regard to all these outcome measures. Results of the AHP are subsequently integrated in a Markov model to make an early assessment of the expected incremental cost-effectiveness of alternative technologies. **RESULTS:** We systematically estimated priors on the clinical effectiveness and wider impacts of the new technology using AHP. In our illustration, AHP estimates for sensitivity and specificity of the new diagnostic technology were used as probability parameters in the Markov model. Moreover, the prioritized outcome measures including clinical effectiveness (weight = 0.61), patient comfort (weight = 0.09), and safety (weight = 0.30) were integrated into one outcome measure in the Markov model. **CONCLUSIONS:** Combining AHP and Markov modelling is particularly valuable in early technology assessment when evidence about the effectiveness of health care technology is still limited or missing. Moreover, combining these methods is valuable when decision makers are interested in other patient relevant outcomes measures besides the technology's clinical effectiveness, and that may not (adequately or explicitly) be captured in mainstream utility measures.

PODIUM SESSION I: RISK-SHARING SCHEMES

RS1

A RISK FORECASTING MODEL TO HELP IN THE DESIGNING OF RISK-SHARING SCHEMES

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OBJECTIVES: To develop a financial risk forecasting model that could be used to negotiate risk-sharing schemes (RSS) conditions. RSS are increasingly being established as a market access strategy and have direct financial implications for both payer and manufacturer. However, underlying methodologies remain poorly researched. Additionally, HTA agencies may need analytical frameworks to evaluate the value of RSS. **METHODS:** We designed a financial-based agreement for a hypothetical technology. The financial risk to be shared is defined as $N \times p \times r$ where N is the size of the target patients population, p is the price/dose of the technology, r is the proportion of patients for whom $di > D$, di being the number of doses/year given to an individual patient i and D being the maximum number of doses/year agreed in the schemes (the cap). a logistic growth curve is used to simulate the risk evolution as time progresses and patients progressively accrue in the RSS. Multiple risk evolution and "sharing" scenarios with their resulting financial implications for both parties are simulated. Finally, a Bayesian framework is introduced to allow both parties to make revisions as real-life information becomes available upon implementation of the RSS. **RESULTS:** For N = 1000 over a period of 3 years, D = 12 and a prior distribution for di centred on 12 doses but with 20% of patients receiving more than 12 doses, the model predicts that 23,092 doses will be delivered and that 542 doses (2.40%) will fall above the cap. These doses in excess determine the cost to be shared: total refund, partial refund, or price discount. **CONCLUSIONS:** Financial modelling and technological forecasting techniques can be combined to simulate different risk-sharing scenarios and their financial implications for payers and manufacturers. This provides both parties with an analytical framework to design win-win schemes and to make potential revisions as real-life information becomes available.

RS2

PAYER ROADBLOCKS TO RISK-SHARING AGREEMENTS AROUND THE WORLD: WHERE, WHEN AND HOW?

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OBJECTIVES: The increasing use of risk-sharing in reimbursement decisions across major markets necessitates that key stakeholders understand the role of this concept in shaping drug development and regulatory decision-making. The objective of this research was to examine global trends in risk-sharing agreements since 1990 to provide a comprehensive understanding of the current and future impact of this fast-evolving concept. **METHODS:** Primary research was conducted through 50 in-depth 45-minute telephone interviews in native languages. Subjects were carefully selected and represented payers, government agencies, and HTA organizations in nine markets (Europe 5, Australia, New Zealand, United States, and Canada) to understand their assessment of the role which risk-sharing agreements have—or have not—played in their respective markets, and whether they will do so in the future. This was complemented with secondary research of reimbursement decisions around the world based on a newly created database of risk-sharing agreements around the world. **RESULTS:** In some countries such as the United Kingdom and Italy, for certain therapeutic areas such as oncology, these agreements almost act as a substitute for the normal reimbursement process, but primary research indicates that this practice faces significant resistance at many layers. Still, many other countries are seeking to understand the potential applicability of risk-shares to their own market. Also, risk-share agreements are being examined for their potential in several other therapeutic areas. While population- and patient-level agreements remain the most popular, we conclude that health outcomes-based arrangements are significantly on the rise, with 27 having been identified through the study in the markets that were studied, the majority of which were signed since 2007. Just over half were signed for oncology therapeutics. **CONCLUSIONS:** Outcomes-based agreements are becoming an increasingly important consideration to include in pricing models across the traditional development pathway for new molecules.